

SEQUENCE LISTING

<110> Maeda, Masatsugu
 Nakata, Yasuhiko
 Nomura, Hitoshi

<120> NOVEL G PROTEIN-COUPLED RECEPTORS

<130> 06501-075001

<140> US 09/807,132

<141> 2001-04-06

<150> PCT/JP99/05578

<151> 1999-10-08

<150> JP 10/288565

<151> 1998-10-09

<150> JP 10/347546

<151> 1998-12-07

<150> JP 10/363537

<151> 1998-12-21

<160> 62

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9)...(947)

<400> 1

ctcattga	atg	gac	agt	cta	aac	caa	aca	aga	gtg	act	gaa	ttt	gtc	ttc	50
	Met	Asp	Ser	Leu	Asn	Gln	Thr	Arg	Val	Thr	Glu	Phe	Val	Phe	
	1				5					10					

ttg	gga	ctc	act	gat	aac	cgg	gtg	ctg	gaa	atg	ctg	ttt	ttc	atg	gca	98
Leu	Gly	Leu	Thr	Asp	Asn	Arg	Val	Leu	Glu	Met	Leu	Phe	Phe	Met	Ala	
15				20					25						30	

ttc	tca	gcc	att	tat	atg	cta	acg	ctt	tca	ggg	aac	att	ctc	atc	atc	146
Phe	Ser	Ala	Ile	Tyr	Met	Leu	Thr	Leu	Ser	Gly	Asn	Ile	Leu	Ile	Ile	
			35					40					45			

att	gcc	aca	gtc	ttt	act	cca	agt	ctc	cat	acc	ccc	atg	tat	ttc	ttc	194
Ile	Ala	Thr	Val	Phe	Thr	Pro	Ser	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	
			50					55					60			

ctg	agc	aat	ctg	tcc	ttt	att	gac	atc	tgc	cac	tca	tct	gtc	act	gtg	242
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Leu	Ser	Asn	Leu	Ser	Phe	Ile	Asp	Ile	Cys	His	Ser	Ser	Val	Thr	Val	
		65					70					75				
cct	aag	atg	ttg	gag	ggg	ttg	ctt	tta	gaa	aga	aag	acc	att	tcc	ttt	290
Pro	Lys	Met	Leu	Glu	Gly	Leu	Leu	Leu	Glu	Arg	Lys	Thr	Ile	Ser	Phe	
	80					85					90					
gac	aac	tgc	atc	aca	cag	ctc	ttc	ttc	cta	cat	ctc	ttt	gcc	tgt	gcc	338
Asp	Asn	Cys	Ile	Thr	Gln	Leu	Phe	Phe	Leu	His	Leu	Phe	Ala	Cys	Ala	
	95				100					105					110	
gag	atc	ttt	ctg	ctg	atc	att	gtg	gcg	tat	gat	cgt	tac	gtg	gct	atc	386
Glu	Ile	Phe	Leu	Leu	Ile	Ile	Val	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	
			115						120					125		
tgc	act	cca	ctc	cac	tac	ccc	aat	gtg	atg	aac	atg	aga	gtc	tgt	ata	434
Cys	Thr	Pro	Leu	His	Tyr	Pro	Asn	Val	Met	Asn	Met	Arg	Val	Cys	Ile	
			130					135					140			
cag	ctt	gtc	ttt	gct	ctc	tgg	ttg	ggg	ggg	act	gtt	cac	tca	cta	ggg	482
Gln	Leu	Val	Phe	Ala	Leu	Trp	Leu	Gly	Gly	Thr	Val	His	Ser	Leu	Gly	
		145					150					155				
cag	acc	ttc	ttg	act	att	cgt	cta	cct	tac	tgt	ggc	ccc	aac	att	att	530
Gln	Thr	Phe	Leu	Thr	Ile	Arg	Leu	Pro	Tyr	Cys	Gly	Pro	Asn	Ile	Ile	
	160					165					170					
gac	agc	tac	ttc	tgt	gat	gtg	cct	ctt	gtt	atc	aag	ctg	gcc	tgc	aca	578
Asp	Ser	Tyr	Phe	Cys	Asp	Val	Pro	Leu	Val	Ile	Lys	Leu	Ala	Cys	Thr	
	175				180					185					190	
gat	aca	tac	ctc	aca	gga	ata	ctg	att	gtg	acc	aat	agt	gga	acc	atc	626
Asp	Thr	Tyr	Leu	Thr	Gly	Ile	Leu	Ile	Val	Thr	Asn	Ser	Gly	Thr	Ile	
				195					200					205		
tcc	ctc	tcc	tgt	ttc	ttg	gcc	gtg	gtc	acc	tcc	tat	atg	gtc	atc	ctg	674
Ser	Leu	Ser	Cys	Phe	Leu	Ala	Val	Val	Thr	Ser	Tyr	Met	Val	Ile	Leu	
			210					215					220			
gtt	tct	ctt	cga	aaa	cac	tca	gct	gaa	ggg	cgc	cag	aaa	gcc	ctg	tct	722
Val	Ser	Leu	Arg	Lys	His	Ser	Ala	Glu	Gly	Arg	Gln	Lys	Ala	Leu	Ser	
		225					230					235				
acc	tgc	tgc	gcc	cac	ttc	atg	gtg	gtt	gcc	ctc	ttc	ttt	ggg	cca	tgt	770
Thr	Cys	Ser	Ala	His	Phe	Met	Val	Val	Ala	Leu	Phe	Phe	Gly	Pro	Cys	
	240					245					250					
atc	ttc	atc	tat	act	cgg	cca	gac	acc	agc	ttc	tcc	att	gac	aag	gtg	818
Ile	Phe	Ile	Tyr	Thr	Arg	Pro	Asp	Thr	Ser	Phe	Ser	Ile	Asp	Lys	Val	
	255				260					265					270	
gtg	tct	gtc	ttc	tac	aca	gtg	gtc	acc	cct	ttg	ctg	aat	ccc	ttc	att	866
Val	Ser	Val	Phe	Tyr	Thr	Val	Val	Thr	Pro	Leu	Leu	Asn	Pro	Phe	Ile	
				275					280					285		
tac	acc	ttg	agg	aat	gag	gag	gta	aaa	agt	gcc	atg	aag	cag	ctc	agg	914
Tyr	Thr	Leu	Arg	Asn	Glu	Glu	Val	Lys	Ser	Ala	Met	Lys	Gln	Leu	Arg	

290	295	300	
cag aga caa gtt ttt ttc acg aaa tca tat aca taatgggcat tgggattgca			967
Gln Arg Gln Val Phe Phe Thr Lys Ser Tyr Thr			
305	310		
gacataattg cagccacatc cttaatgaaa gagcaaaagt aaagagtcaa aatcaactta			1027
tataacttgg taaattaggt aaaatggcat agagcaggtc agatttctgc tcattaaaga			1087
taagaactta ttctgttcat taaagataag aacttattaa ctattattta aataaa			1143
<210> 2			
<211> 1248			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (13)...(951)			
<400> 2			
attctctgagg at atg gaa aga atc aac agc aca ctg ttg act gcg ttt atc			51
Met Glu Arg Ile Asn Ser Thr Leu Leu Thr Ala Phe Ile			
1	5	10	
ctg aca gga att ccg tat cca ctc agg cta agg aca ctc ttt ttt gtg			99
Leu Thr Gly Ile Pro Tyr Pro Leu Arg Leu Arg Thr Leu Phe Phe Val			
15	20	25	
ttc ttt ttt cta atc tac atc ctg act cag ctg gga aac ctg ctt att			147
Phe Phe Phe Leu Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile			
30	35	40	45
tta atc act gtc tgg gca gac cca agg ctc cat gcc cgc ccc atg tac			195
Leu Ile Thr Val Trp Ala Asp Pro Arg Leu His Ala Arg Pro Met Tyr			
50	55	60	
atc ttt ctt ggt gtt ctc tca gtc att gat atg agc atc tcc tcc atc			243
Ile Phe Leu Gly Val Leu Ser Val Ile Asp Met Ser Ile Ser Ser Ile			
65	70	75	
att gtc cct cgc ctc atg atg aac ttc act tta ggt gtc aaa ccc atc			291
Ile Val Pro Arg Leu Met Met Asn Phe Thr Leu Gly Val Lys Pro Ile			
80	85	90	
cca ttt ggt ggc tgt gtt gct caa ctc tat ttc tat cac ttc ctg ggc			339
Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly			
95	100	105	
agc acc cag tgc ttc ctc tac acc cta atg gcc tat gac agg tac ctg			387
Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu			
110	115	120	125
gca ata tgt cag ccc ctg cgc tac cct gtg ctc atg act gct aag ctg			435
Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Thr Ala Lys Leu			
130	135	140	
agc gcc ttg ctt gtg gct gga gcc tgg atg gca gga tcc atc cat ggg			483

Ser	Ala	Leu	Leu	Val	Ala	Gly	Ala	Trp	Met	Ala	Gly	Ser	Ile	His	Gly		
			145					150					155				
gct	ctc	cag	gcc	atc	cta	acc	ttc	cgc	ctg	ccc	tac	tgt	ggg	ccc	aat	531	
Ala	Leu	Gln	Ala	Ile	Leu	Thr	Phe	Arg	Leu	Pro	Tyr	Cys	Gly	Pro	Asn		
		160					165					170					
cag	gtg	gat	tac	ttc	ttc	tgt	gac	atc	cct	gca	gtg	ttg	aga	ctg	gcc	579	
Gln	Val	Asp	Tyr	Phe	Phe	Cys	Asp	Ile	Pro	Ala	Val	Leu	Arg	Leu	Ala		
		175				180					185						
tgt	gct	gac	aca	aca	gtc	aac	gag	ctg	gtg	acg	ttt	gta	gac	att	ggg	627	
Cys	Ala	Asp	Thr	Thr	Val	Asn	Glu	Leu	Val	Thr	Phe	Val	Asp	Ile	Gly		
190					195				200						205		
gtg	gtg	gtt	gcc	agt	tgc	ttc	tcc	ctg	atc	ctc	ctc	tcc	tac	ata	cag	675	
Val	Val	Val	Ala	Ser	Cys	Phe	Ser	Leu	Ile	Leu	Leu	Ser	Tyr	Ile	Gln		
				210					215					220			
atc	att	cag	gcc	atc	ctg	aga	atc	cac	aca	gct	gat	ggg	cgg	cgc	cgg	723	
Ile	Ile	Gln	Ala	Ile	Leu	Arg	Ile	His	Thr	Ala	Asp	Gly	Arg	Arg	Arg		
			225					230					235				
gct	ttt	tca	act	tgt	gga	gcc	cat	gta	acc	gtg	gtc	acc	gtg	tac	tat	771	
Ala	Phe	Ser	Thr	Cys	Gly	Ala	His	Val	Thr	Val	Val	Thr	Val	Tyr	Tyr		
		240					245					250					
gtg	ccc	tgt	gcc	ttc	atc	tac	ctg	agg	cct	gaa	acc	aac	agc	ccc	ctg	819	
Val	Pro	Cys	Ala	Phe	Ile	Tyr	Leu	Arg	Pro	Glu	Thr	Asn	Ser	Pro	Leu		
	255					260					265						
gat	ggg	gca	gct	gcc	cta	gtc	ccc	acg	gcc	atc	act	cct	ttc	ctc	aac	867	
Asp	Gly	Ala	Ala	Ala	Leu	Val	Pro	Thr	Ala	Ile	Thr	Pro	Phe	Leu	Asn		
					275					280					285		
ccc	ctt	atc	tac	act	ctg	cgg	aac	caa	gag	gtg	aag	ctg	gcc	ctg	aaa	915	
Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn	Gln	Glu	Val	Lys	Leu	Ala	Leu	Lys		
				290				295						300			
aga	atg	ctc	aga	agc	cca	aga	act	ccg	agt	gag	gtt	tgaaagtgtc				961	
Arg	Met	Leu	Arg	Ser	Pro	Arg	Thr	Pro	Ser	Glu	Val						
		305					310										
tttctccac	tagggaagct	gccacaatta	gaatttatta	taatgttttag	gcttcggtaa	1021											
cttttttctt	ttcttcttgt	tttttctctt	ttatatagcc	atactgtatg	atcaaacaca	1081											
gtttaaggta	aaatactaac	tttctaacag	ttccttagta	tcctctcaag	ataactctca	1141											
gccactgcaa	gagtagagaa	tgagacaaaa	ttctcacaaa	ctaaaccaca	ttaaacaatc	1201											
cagaagaaag	aatgcaatag	tgtattttcc	aatgtctcag	taataaaa		1248											

<210> 3

<211> 1431

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (410)...(1339)

<400> 3

ggcaacctaa aagcaagcat ggacagttcc ttggtgaata accaaaaaca agatggagtc 60
 tcgctctgtt gcccaggctg gagtgtagtg ggcgcctctc ggctcgctgc ggtctccgcc 120
 tcccgggttc aggcgattct ccggcctcag cctcccgggt gcgtgggatt gcaggaacta 180
 gaactaaagc gaggttaatt tccacagtga gaacatgctc cagacatccg agcaccagtg 240
 tggctctgga aactccacag ataccacagg actagaaaaat aactggacaa tgggatgttc 300
 tatcttgccc gaactgaggg atataaaaag ctccaaagac aaagaaagta ccatccaccc 360
 atcccaaaag aaattatcct tccttctgaa aataagactg caaaaagac atg gga aag 418
 Met Gly Lys
 1

acc aaa aac aca tcg ctg gat gcc gtg gtg aca gat ttc att ctt ctg 466
 Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe Ile Leu Leu
 5 10 15

ggt ttg tct cac ccc cca aat cta aga agc ctc ctc ttc ctg gtc ttc 514
 Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Phe Leu Val Phe
 20 25 30 35

ttc atc att tac atc ctc act cag ctg ggg aac ctg ctc att ctg ctc 562
 Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Leu
 40 45 50

acc atg tgg gct gac ccg aag ctc tgt gct cgc ccc atg tac att ctt 610
 Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met Tyr Ile Leu
 55 60 65

ctg gga gtg ctc tca ttc ctg gac atg tgg ctc tcc tca gtc acc gtt 658
 Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser Val Thr Val
 70 75 80

cct cgg ctt att ttg gat ttt act cct tcc atc aag gct atc ccg ttt 706
 Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala Ile Pro Phe
 85 90 95

ggt ggc tgt gtg gct caa ctg tat ttc ttt cac ttc ctg ggc agc acc 754
 Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr
 100 105 110 115

cag tgc ttc ctc tac acc ttg atg gcc tat gac agg tac cta gca ata 802
 Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile
 120 125 130

tgt cag ccc ctg cac tac cca gtg ctc atg aat ggg agg tta tgc aca 850
 Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg Leu Cys Thr
 135 140 145

gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc atg cat ggg tct atc 898
 Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His Gly Ser Ile
 150 155 160

cag gcc acc ttg acc ttc cgc ctg ccc tac tgt ggg ccc aat cag gtg 946
 Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val
 165 170 175

gat tac ttt atc tgt gac atc cgc gca gta ttg aga ctg gcc tgt gct 994

Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu Ala Cys Ala
 180 185 190 195
 gac aca act gtc aat gag ctt gtg acc ttt gtg gac gtc agg gta gtg 1042
 Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val Arg Val Val
 200 205 210
 gcc gcc agt tgc ttc atg tta att ctg ctc tcc tat gcc aac ata gtc 1090
 Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala Asn Ile Val
 215 220 225
 cat gcc atc ctg aag ata cgc acc gct gat ggg agg cgc cgg gcc ttc 1138
 His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg Arg Ala Phe
 230 235 240
 tcc acc tgt ggc tcc cac cta atc gtg gtc aca gtc tac tat gtc ccc 1186
 Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr Tyr Val Pro
 245 250 255
 tgt att ttc atc tac ctt agg gct ggc tcc aaa gac ccc ctg gat ggg 1234
 Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro Leu Asp Gly
 260 265 270 275
 gca gcg gct gtg ttt tac act gtt gtc act cca tta ctg aac ccc ctc 1282
 Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu
 280 285 290
 atc tat aca ctg agg aac cag gaa gtg aag tct gcc ctg aag agg ata 1330
 Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu Lys Arg Ile
 295 300 305
 aca gca ggt tgaaggactg aatgaaaata agtaactaca tctgcatcat 1379
 Thr Ala Gly
 310
 tatcactgcc actctcttca gctactgctg catgtgacaa atgcccaata aa 1431

<210> 4

<211> 313

<212> PRT

<213> Homo sapiens

<400> 4

Met Asp Ser Leu Asn Gln Thr Arg Val Thr Glu Phe Val Phe Leu Gly
 1 5 10 15
 Leu Thr Asp Asn Arg Val Leu Glu Met Leu Phe Phe Met Ala Phe Ser
 20 25 30
 Ala Ile Tyr Met Leu Thr Leu Ser Gly Asn Ile Leu Ile Ile Ala
 35 40 45
 Thr Val Phe Thr Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ile Asp Ile Cys His Ser Ser Val Thr Val Pro Lys
 65 70 75 80
 Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe Asp Asn
 85 90 95
 Cys Ile Thr Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ala Glu Ile
 100 105 110

```

Phe Leu Leu Ile Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Thr
    115                120                125
Pro Leu His Tyr Pro Asn Val Met Asn Met Arg Val Cys Ile Gln Leu
    130                135                140
Val Phe Ala Leu Trp Leu Gly Gly Thr Val His Ser Leu Gly Gln Thr
    145                150                155                160
Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile Asp Ser
    165                170                175
Tyr Phe Cys Asp Val Pro Leu Val Ile Lys Leu Ala Cys Thr Asp Thr
    180                185                190
Tyr Leu Thr Gly Ile Leu Ile Val Thr Asn Ser Gly Thr Ile Ser Leu
    195                200                205
Ser Cys Phe Leu Ala Val Val Thr Ser Tyr Met Val Ile Leu Val Ser
    210                215                220
Leu Arg Lys His Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser Thr Cys
    225                230                235                240
Ser Ala His Phe Met Val Val Ala Leu Phe Phe Gly Pro Cys Ile Phe
    245                250                255
Ile Tyr Thr Arg Pro Asp Thr Ser Phe Ser Ile Asp Lys Val Val Ser
    260                265                270
Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Thr
    275                280                285
Leu Arg Asn Glu Glu Val Lys Ser Ala Met Lys Gln Leu Arg Gln Arg
    290                295                300
Gln Val Phe Phe Thr Lys Ser Tyr Thr
    305                310

```

<210> 5

<211> 313

<212> PRT

<213> Homo sapiens

<400> 5

```

Met Glu Arg Ile Asn Ser Thr Leu Leu Thr Ala Phe Ile Leu Thr Gly
    1                5                10                15
Ile Pro Tyr Pro Leu Arg Leu Arg Thr Leu Phe Phe Val Phe Phe Phe
    20                25                30
Leu Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Ile Thr
    35                40                45
Val Trp Ala Asp Pro Arg Leu His Ala Arg Pro Met Tyr Ile Phe Leu
    50                55                60
Gly Val Leu Ser Val Ile Asp Met Ser Ile Ser Ser Ile Ile Val Pro
    65                70                75                80
Arg Leu Met Met Asn Phe Thr Leu Gly Val Lys Pro Ile Pro Phe Gly
    85                90                95
Gly Cys Val Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly Ser Thr Gln
    100               105               110
Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys
    115               120               125
Gln Pro Leu Arg Tyr Pro Val Leu Met Thr Ala Lys Leu Ser Ala Leu
    130               135               140
Leu Val Ala Gly Ala Trp Met Ala Gly Ser Ile His Gly Ala Leu Gln
    145               150               155               160
Ala Ile Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp
    165               170               175
Tyr Phe Phe Cys Asp Ile Pro Ala Val Leu Arg Leu Ala Cys Ala Asp
    180               185               190

```

```

Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile Gly Val Val Val
    195                200                205
Ala Ser Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln Ile Ile Gln
    210                215                220
Ala Ile Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser
225                230                235                240
Thr Cys Gly Ala His Val Thr Val Val Thr Val Tyr Tyr Val Pro Cys
    245                250                255
Ala Phe Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu Asp Gly Ala
    260                265                270
Ala Ala Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile
    275                280                285
Tyr Thr Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys Arg Met Leu
    290                295                300
Arg Ser Pro Arg Thr Pro Ser Glu Val
305                310

```

<210> 6

<211> 310

<212> PRT

<213> Homo sapiens

<400> 6

```

Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe
 1                5                10                15
Ile Leu Leu Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Phe
    20                25                30
Leu Val Phe Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu
    35                40                45
Ile Leu Leu Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met
    50                55                60
Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser
65                70                75                80
Val Thr Val Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala
    85                90                95
Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu
    100                105                110
Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr
    115                120                125
Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg
    130                135                140
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His
145                150                155                160
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
    165                170                175
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu
    180                185                190
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val
    195                200                205
Arg Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
    210                215                220
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg
225                230                235                240
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
    245                250                255
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro
    260                265                270

```


Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
 275 280 285
 Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu
 290 295 300
 Lys Arg Ile Thr Ala Gly
 305 310

<210> 7
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 7
 atggacagtc taaaccaaac aagagtg 27

<210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 8
 atggcattct cagccattta tatgcta 27

<210> 9
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 9
 gggaacattc tcatcatcat tgccaca 27

<210> 10
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 10
 ttatgtatat gatttcgtga aaaaaac 27

<210> 11
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 11

tacctcctca ttcctcaagg tgtaa

27

<210> 12

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 12

ggtgaccact gtgtagaaga cagacac

27

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 13

atggaaagaa tcaacagcac actgttg

27

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 14

tctaattctac atcctgactc agctggg

27

<210> 15

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 15

ttcaaacctc actcggagtt cttgggc

27

<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 16
 agcttcacct cttggttccg cagagtg 27

 <210> 17
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 17
 atgggaaaga ccaaaaacac atcgctg 27

 <210> 18
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 18
 cgtggtgaca gatttcattc ttctggg 27

 <210> 19
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 19
 tcaacctgct gttatcctct tcagggc 27

 <210> 20
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 20
 cctggttcct cagtgtatag atgaggg 27

 <210> 21
 <211> 942
 <212> DNA
 <213> Homo sapiens

 <400> 21
 atggacagtc taaaccaaac aagagtgact gaatttgtct tcttgggact cactgataac 60
 cgggtgctgg aaatgctgtt ttcatggca ttctcagcca tttatatgct aacgctttca 120
 gggaacattc tcatcatcat tgccacagtc ttactccaa gtctccatac ccccatgtat 180
 ttcttctga gcaatctgtc ctttattgac atctgccact catctgtcac tgtgcctaag 240

atgttggagg	gtttgctttt	agaaagaaag	accatttcct	ttgacaactg	catcacacag	300
ctcttcttcc	tacatctctt	tgcctgtgcc	gagatctttc	tgctgatcat	tgtggcgtat	360
gatcgttacg	tggctatctg	cactccactc	cactaccca	atgtgatgaa	catgagagtc	420
tgtatacagc	ttgtctttgc	tctctggttg	gggggtactg	ttcactcact	agggcagacc	480
ttcttgacta	ttcgtctacc	ttactgtggc	cccaacatta	ttgacagcta	cttctgtgat	540
gtgcctcttg	ttatcaagct	ggcctgcaca	gatacatacc	tcacaggaat	actgattgtg	600
accaatagtg	gaaccatctc	cctctcctgt	ttcttggccg	tggtcacctc	ctatatggtc	660
atcctggttt	ctcttcgaaa	acactcagct	gaaggcgcc	agaaagccct	gtctacctgc	720
tcggcccact	tcatggtggt	tgcctcttcc	tttgggccat	gtatcttcat	ctatactcgg	780
ccagacacca	gcttctccat	tgacaagggtg	gtgtctgtct	tctacacagt	ggtcacccct	840
ttgctgaatc	ccttcattta	caccttgagg	aatgaggagg	taaaaagtgc	catgaagcag	900
ctcaggcaga	gacaagtttt	tttcacgaaa	tcatatacat	aa		942

<210> 22

<211> 942

<212> DNA

<213> Homo sapiens

<400> 22

atggaaagaa	tcaacagcac	actggtgact	gcgtttatcc	tgacaggaat	tccgtatcca	60
ctcaggctaa	ggacactett	ttttgtgttc	ttttttctaa	tctacatcct	gactcagctg	120
ggaaacctgc	ttattttaat	cactgtctgg	gcagacccaa	ggctccatgc	ccgccccatg	180
tacatctttc	ttggtgttct	ctcagtcatt	gatatgagca	tctcctccat	cattgtccct	240
cgccctcatga	tgaacttcac	tttaggtgtc	aaacccatcc	catttggtgg	ctgtgttgct	300
caactctatt	tctatcaact	cctgggcagc	acccagtgtc	tcctctacac	cctaattggcc	360
tatgacaggt	acctggcaat	atgtcagccc	ctgcgtacc	ctgtgctcat	gactgctaag	420
ctgagcgcc	tgttgtgtgc	tggagcctgg	atggcaggat	ccatccatgg	ggctctccag	480
gccatcttaa	ccttcgcct	gccctactgt	gggccaatc	aggtggatta	cttcttctgt	540
gacatccctg	cagtgttgag	actggcctgt	gctgacacaa	cagtcaacga	gctggtgacg	600
tttgtagaca	ttggggtggt	ggttgccagt	tgcttctccc	tgatcctcct	ctcctacata	660
cagatcattc	aggccatcct	gagaatccac	acagctgatg	ggcggcgccg	ggctttttca	720
acttgtggag	cccatgtaac	cgtggtcacc	gtgtactatg	tgccctgtgc	cttcatctac	780
ctgaggcctg	aaaccaacag	ccccctggat	ggggcagctg	ccctagtccc	cacggccatc	840
actcctttcc	tcaaccccc	tatctacact	ctgcggaacc	aagagggtgaa	gctggccctg	900
aaaagaatgc	tcagaagccc	aagaactccg	agtgaggttt	ga		942

<210> 23

<211> 933

<212> DNA

<213> Homo sapiens

<400> 23

atgggaaaga	ccaaaaacac	atcgctggat	gccgtggtga	cagatttcat	tcttctgggt	60
ttgtctcacc	cccccattct	aagaagcctc	ctcttcctgg	tcttcttcat	catttacatc	120
ctcactcagc	tggggaacct	gtcatttctg	ctcaccatgt	gggctgaccc	gaagctctgt	180
gctcgcccca	tgtacattct	tctgggagtg	ctctcattcc	tggacatgtg	gctctcctca	240
gtcaccgttc	ctcggtttat	tttggatttt	actccttcca	tcaaggctat	cccgtttggt	300
ggctgtgtgg	ctcaactgta	tttctttcac	ttcctgggca	gcacccagtg	cttctctac	360
accttgatgg	cctatgacag	gtacctagca	atatgtcagc	ccctgcacta	cccagtgtct	420
atgaatggga	ggttatgcac	agtccttgtg	gctggagctt	gggtcgccgg	ctccatgcat	480
gggtctatcc	aggccacctt	gaccttccgc	ctgcctact	gtgggcccac	tcagggtgat	540
tactttatct	gtgacatccg	cgcagtattg	agactggcct	gtgctgacac	aactgtcaat	600
gagcttgtga	cctttgtgga	cgtcagggtg	gtggccgcca	gttgcttcat	gttaattctg	660
ctctcctatg	ccaacatagt	ccatgccatc	ctgaagatac	gcaccgctga	tgggagcgcg	720
cgggccttct	ccacctgtgg	ctcccaccta	atcggtgtca	cagtctacta	tgtcccctgt	780
atthtcatct	accttagggc	tggctccaaa	gacccctgg	atggggcagc	ggctgtgttt	840
tacactgttg	tactccatt	actgaacccc	ctcatctata	cactgaggaa	ccaggaagtg	900

aagtctgccc tgaagaggat aacagcaggt tga 933

<210> 24

<211> 1060

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (17)...(892)

<400> 24

aaatgcctaa agaaga atg acc atg gaa aat tat tct atg gca gct cag ttt 52

Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe

1

5

10

gtc tta gat ggt tta aca cag caa gca gag ctc cag ctg ccc ctc ttc 100

Val Leu Asp Gly Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe

15

20

25

ctc ctg ttc ctg gga atc tat gtg gtc aca gta gtg ggc aac ctg ggc 148

Leu Leu Phe Leu Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly

30

35

40

atg att ctc ctg att gca gtc agc cct cta ctt cac acc ccc atg tac 196

Met Ile Leu Leu Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr

45

50

55

60

tat ttc ctc agc agc ttg tcc ttc gtc gat ttc tgc tat tcc tct gtc 244

Tyr Phe Leu Ser Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val

65

70

75

att act ccc aaa atg ctg gtg aac ttc cta gga aag aag aat aca atc 292

Ile Thr Pro Lys Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile

80

85

90

ctt tac tct gag tgc atg gtc cag ctc ttt ttc ttt gtg gtc ttt gtg 340

Leu Tyr Ser Glu Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val

95

100

105

gtg gct gag ggt tac ctc ctg act gcc atg gca tat gat cgc tat gtt 388

Val Ala Glu Gly Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val

110

115

120

gcc atc tgt agc cca ctg ctt tat aat gcg atc atg tcc tca tgg gtc 436

Ala Ile Cys Ser Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val

125

130

135

140

tgc tca ctg cta gtg ctg gct gcc ttc ttc ttg ggc ttt ctc tct gcc 484

Cys Ser Leu Leu Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala

145

150

155

ttg act cat aca agt gcc atg atg aaa ctg tcc ttt tgc aaa tcc cac 532

Leu Thr His Thr Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His

160

165

170

att atc aac cat tac ttc tgt gat gtt ctt ccc ctc ctc aat ctc tcc 580

Ile Ile Asn His Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser	
175 180 185	
tgc tcc aac aca cac ctc aat gag ctt cta ctt ttt atc att gcg ggg	628
Cys Ser Asn Thr His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly	
190 195 200	
ttt aac acc ttg gtg ccc acc cta gct gtt gct gtc tcc tat gcc ttc	676
Phe Asn Thr Leu Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe	
205 210 215 220	
atc ctc tac agc atc ctt cac atc cgc tcc tca gag ggc cgg tcc aaa	724
Ile Leu Tyr Ser Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys	
225 230 235	
gct ttt gga aca tgc agc tct cat ctc atg gct gtg gtg atc ttc ttt	772
Ala Phe Gly Thr Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe	
240 245 250	
ggg tcc att acc ttc atg tat ttc aag ccc cct tca agt aac tcc ctg	820
Gly Ser Ile Thr Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu	
255 260 265	
gac cag gag aag gtg tcc tct gtg ttc tac acc acg gtg atc ccc atg	868
Asp Gln Glu Lys Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met	
270 275 280	
ctg aac cct tta ata tac agt ctg taatcacagc actttggaag gctgaggcag	922
Leu Asn Pro Leu Ile Tyr Ser Leu	
285 290	
ggttgcttga gtccagtttg agaccatcct gggaacata gtgcgatctt gtttctttcc	982
actgcctaaa aacttcaatg ctcaatttta cttgcaattt cctcttctctg acatggagaa	1042
tgttggttg gaatgttc	1060
<210> 25	
<211> 1069	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (18)...(956)	
<400> 25	
atttttgaag acaaaaa atg ctg gct aga aac aac tcc tta gtg act gaa	50
Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu	
1 5 10	
ttt att ctt gct gga tta aca gat cgt cca gag ttc tgg caa ccc ttc	98
Phe Ile Leu Ala Gly Leu Thr Asp Arg Pro Glu Phe Trp Gln Pro Phe	
15 20 25	
ttt ttc ctg ttc cta gtg atc tac att gtc acc atg gta ggc aac ctt	146
Phe Phe Leu Phe Leu Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu	
30 35 40	

ggc ttg atc act ctt ttc ggt cta aat tct cac ctc cac aca cca atg Gly Leu Ile Thr Leu Phe Gly Leu Asn Ser His Leu His Thr Pro Met 45 50 55	194
tac tat ttc ctc ttc aat ctc tcc ttc att gat ctc tgt tac tcc tct Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser 60 65 70 75	242
gtt ttc act ccc aaa atg cta atg aac ttt gtg tca aaa aag aat att Val Phe Thr Pro Lys Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile 80 85 90	290
atc tcc aat gtt ggg tgc atg act cgg ctg ttt ttc ttt ctc ttt ttc Ile Ser Asn Val Gly Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe 95 100 105	338
gtc atc tct gaa tgt tac atg ttg acc tca atg gca tat gat cgc tat Val Ile Ser Glu Cys Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr 110 115 120	386
gtg gcc atc tgt aat cca ttg ctg tat aag gtc acc atg tcc cat cag Val Ala Ile Cys Asn Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln 125 130 135	434
gtc tgt tct atg ctc act ttt gct gct tac ata atg gga ttg gct gga Val Cys Ser Met Leu Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly 140 145 150 155	482
gcc acg gcc cac acc ggg tgc atg ttt aga ctc acc ttc tgc agt gct Ala Thr Ala His Thr Gly Cys Met Phe Arg Leu Thr Phe Cys Ser Ala 160 165 170	530
aat atc att aac cat tac ttg tgt gac ata ctc ccc ctc ctc cag ctt Asn Ile Ile Asn His Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu 175 180 185	578
tcc tgc acc agc acc tat gtc aac gag gtg gtt gtt ctc att gtt gtg Ser Cys Thr Ser Thr Tyr Val Asn Glu Val Val Val Leu Ile Val Val 190 195 200	626
ggc act aat atc acg gta ccc agt tgt acc atc ctc att tct tat gtt Gly Thr Asn Ile Thr Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val 205 210 215	674
ttc att gtc act agc att ctt cat atc aaa tcc act caa gga aga tca Phe Ile Val Thr Ser Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser 220 225 230 235	722
aaa gcc ttc agt act tgt agc tct cat gtc att gct ctg tct ctg ttt Lys Ala Phe Ser Thr Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe 240 245 250	770
ttt ggg tca gcg gca ttc atg tat att aaa tat tct tct gga tct atg Phe Gly Ser Ala Ala Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met 255 260 265	818
gag cag gga aaa gtt ttt tct gtt ttc tac act aat gtg gtg ccc atg	866

Glu Gln Gly Lys Val Phe Ser Val Phe Tyr Thr Asn Val Val Pro Met	
270 275 280	
ctc aat ccc ctc atc tac agt ttg agg aac aag gat gtc aaa gtt gca	914
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala	
285 290 295	
ctg agg aaa gct ctg att aaa att cag agg aga aat ata ttc	956
Leu Arg Lys Ala Leu Ile Lys Ile Gln Arg Arg Asn Ile Phe	
300 305 310	
taattagaag cagtaatgat gtaaaacaat tgaaggactt caaattttta ttagtgtttt	1016
tcatgaagag attttgttgt ttctacagat ggtgttatgt gtgatttaaat aaa	1069
<210> 26	
<211> 1069	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (18)...(956)	
<400> 26	
atttttgaag acaaaaa atg ctg gct aga aac aac tcc tta gtg act gaa	50
Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu	
1 5 10	
ttt att ctt gct gga tta aca gat cgt cca gag ttc cgg caa ccc ctc	98
Phe Ile Leu Ala Gly Leu Thr Asp Arg Pro Glu Phe Arg Gln Pro Leu	
15 20 25	
ttt ttc ctg ttt cta gtg atc tac att gtc acc atg gta ggc aac ctt	146
Phe Phe Leu Phe Leu Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu	
30 35 40	
ggc ttg atc att ctt ttc ggt cta aat tct cac ctc cac aca cca atg	194
Gly Leu Ile Ile Leu Phe Gly Leu Asn Ser His Leu His Thr Pro Met	
45 50 55	
tac tat ttc ctc ttc aat ctc tcc ttc att gat ctc tgt tac tcc tct	242
Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser	
60 65 70 75	
gtt ttc act ccc aaa atg cta atg aac ttt gta tca aaa aag aat att	290
Val Phe Thr Pro Lys Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile	
80 85 90	
atc tcc tat gtt ggg tgc atg act cag ctg ttt ttc ttt ctc ttt ttt	338
Ile Ser Tyr Val Gly Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe	
95 100 105	
gtc atc tct gaa tgc tac ata ttg acc tca atg gca tat gat cgc tat	386
Val Ile Ser Glu Cys Tyr Ile Leu Thr Ser Met Ala Tyr Asp Arg Tyr	
110 115 120	
gtg gcc atc tgt aat cca ttg ctg tat aag gtc acc atg tcc cat cag	434

[illegible]

```
<210> 27
<211> 976
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS

<222> (19)...(945)

<400> 27

acagctcgcc aagagaga atg act ctg aga aac agc tcc tca gtg act gag	51
Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu	
1 5 10	
ttt atc ctt gtg gga tta tca gaa cag cca gag ctc cag ctc cct ctt	99
Phe Ile Leu Val Gly Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu	
15 20 25	
ttc ctt cta ttc tta ggg atc tat gtg ttc act gtg gtg ggc aac ttg	147
Phe Leu Leu Phe Leu Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu	
30 35 40	
ggc ttg atc acc tta att ggg ata aat cct agc ctt cac acc ccc atg	195
Gly Leu Ile Thr Leu Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met	
45 50 55	
tac ttt ttc ctc ttc aac ttg tcc ttt ata gat ctc tgt tat tcc tgt	243
Tyr Phe Phe Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys	
60 65 70 75	
gtg ttt acc ccc aaa atg ctg aat gac ttt gtt tca gaa agt atc atc	291
Val Phe Thr Pro Lys Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile	
80 85 90	
tct tat gtg gga tgt atg act cag cta ttt ttc ttc tgt ttc ttt gtc	339
Ser Tyr Val Gly Cys Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val	
95 100 105	
aat tct gag tgc tat gtg ttg gta tca atg gcc tat gat cgc tat gtg	387
Asn Ser Glu Cys Tyr Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val	
110 115 120	
gcc atc tgc aac ccc ctg ctc tac atg gtc acc atg tcc cca agg gtc	435
Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val	
125 130 135	
tgc ttt ctg ctg atg ttt ggt tcc tat gtg gta ggg ttt gct ggg gcc	483
Cys Phe Leu Leu Met Phe Gly Ser Tyr Val Val Gly Phe Ala Gly Ala	
140 145 150 155	
atg gcc cac act gga agc atg ctg cga ctg acc ttc tgt gat tcc aac	531
Met Ala His Thr Gly Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn	
160 165 170	
gtc att gac cat tat ctg tgt gac gtt ctc ccc ctc ttg cag ctc tcc	579
Val Ile Asp His Tyr Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser	
175 180 185	
tgc acc agc acc cat gtc agt gag ctg gta ttt ttc att gtt gtt gga	627
Cys Thr Ser Thr His Val Ser Glu Leu Val Phe Phe Ile Val Val Gly	
190 195 200	
gta atc acc atg cta tcc agc ata agc atc gtc atc tct tac gct ttg	675
Val Ile Thr Met Leu Ser Ser Ile Ser Ile Val Ile Ser Tyr Ala Leu	

205	210	215	
ata ctc tcc aac atc ctc tgt att cct tct gca gag ggc aga tcc aaa			723
Ile Leu Ser Asn Ile Leu Cys Ile Pro Ser Ala Glu Gly Arg Ser Lys			
220	225	230	235
gcc ttt agc aca tgg ggc tcc cac ata att gct gtt gct ctg ttt ttt			771
Ala Phe Ser Thr Trp Gly Ser His Ile Ile Ala Val Ala Leu Phe Phe			
	240	245	250
ggg tca ggg aca ttc acc tac tta aca aca tct ttt cct ggc tct atg			819
Gly Ser Gly Thr Phe Thr Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met			
	255	260	265
aac cat ggc aga ttt gcc tca gtc ttt tac acc aat gtg gtt ccc atg			867
Asn His Gly Arg Phe Ala Ser Val Phe Tyr Thr Asn Val Val Pro Met			
	270	275	280
ctt aac cct tcg atc tac agt ttg agg aat aag gat gat aaa ctt gcc			915
Leu Asn Pro Ser Ile Tyr Ser Leu Arg Asn Lys Asp Asp Lys Leu Ala			
	285	290	295
ctg ggc aaa acc ctg aag aga gtg ctc ttc taatgggtct cttcatatca			965
Leu Gly Lys Thr Leu Lys Arg Val Leu Phe			
300	305		
ctggcaaccg a			976
<210> 28			
<211> 292			
<212> PRT			
<213> Homo sapiens			
<400> 28			
Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly			
1 5 10 15			
Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu			
20 25 30			
Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu			
35 40 45			
Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser			
50 55 60			
Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys			
65 70 75 80			
Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu			
85 90 95			
Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly			
100 105 110			
Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser			
115 120 125			
Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu			
130 135 140			
Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr			
145 150 155 160			
Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His			
165 170 175			
Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr			

```

      180      185      190
His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu
      195      200      205
Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser
      210      215      220
Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
225      230      235
Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr
      245      250      255
Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys
      260      265      270
Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu
      275      280      285
Ile Tyr Ser Leu
      290

```

```

<210> 29
<211> 313
<212> PRT
<213> Homo sapiens

```

```

<400> 29
Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly
 1      5      10      15
Leu Thr Asp Arg Pro Glu Phe Trp Gln Pro Phe Phe Phe Leu Phe Leu
      20      25      30
Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Thr Leu
      35      40      45
Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe
      50      55      60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
      65      70      75      80
Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Asn Val Gly
      85      90      95
Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys
      100      105      110
Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115      120      125
Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu
      130      135      140
Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr
      145      150      155      160
Gly Cys Met Phe Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His
      165      170      175
Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
      180      185      190
Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Thr Asn Ile Thr
      195      200      205
Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
      210      215      220
Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
      225      230      235      240
Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
      245      250      255
Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
      260      265      270
Phe Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile

```

	275		280		285
Tyr	Ser	Leu	Arg	Asn	Lys
	290			295	
Ile	Lys	Ile	Gln	Arg	Arg
305				310	

<210> 30
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 30															
Met	Leu	Ala	Arg	Asn	Asn	Ser	Leu	Val	Thr	Glu	Phe	Ile	Leu	Ala	Gly
1				5					10					15	
Leu	Thr	Asp	Arg	Pro	Glu	Phe	Arg	Gln	Pro	Leu	Phe	Phe	Leu	Phe	Leu
		20						25					30		
Val	Ile	Tyr	Ile	Val	Thr	Met	Val	Gly	Asn	Leu	Gly	Leu	Ile	Ile	Leu
		35					40					45			
Phe	Gly	Leu	Asn	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Tyr	Phe	Leu	Phe
	50					55					60				
Asn	Leu	Ser	Phe	Ile	Asp	Leu	Cys	Tyr	Ser	Ser	Val	Phe	Thr	Pro	Lys
65					70					75					80
Met	Leu	Met	Asn	Phe	Val	Ser	Lys	Lys	Asn	Ile	Ile	Ser	Tyr	Val	Gly
			85						90					95	
Cys	Met	Thr	Gln	Leu	Phe	Phe	Phe	Leu	Phe	Phe	Val	Ile	Ser	Glu	Cys
			100					105						110	
Tyr	Ile	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Asn
		115					120					125			
Pro	Leu	Leu	Tyr	Lys	Val	Thr	Met	Ser	His	Gln	Val	Cys	Ser	Met	Leu
	130					135					140				
Thr	Phe	Ala	Ala	Tyr	Ile	Met	Gly	Leu	Ala	Gly	Ala	Thr	Ala	His	Thr
145					150					155					160
Gly	Cys	Met	Leu	Arg	Leu	Thr	Phe	Cys	Ser	Ala	Asn	Ile	Ile	Asn	His
			165					170						175	
Tyr	Leu	Cys	Asp	Ile	Leu	Pro	Leu	Leu	Gln	Leu	Ser	Cys	Thr	Ser	Thr
		180					185					190			
Tyr	Val	Asn	Glu	Val	Val	Val	Leu	Ile	Val	Val	Gly	Ile	Asn	Ile	Met
		195					200				205				
Val	Pro	Ser	Cys	Thr	Ile	Leu	Ile	Ser	Tyr	Val	Phe	Ile	Val	Thr	Ser
	210					215					220				
Ile	Leu	His	Ile	Lys	Ser	Thr	Gln	Gly	Arg	Ser	Lys	Ala	Phe	Ser	Thr
225				230						235					240
Cys	Ser	Ser	His	Val	Ile	Ala	Leu	Ser	Leu	Phe	Phe	Gly	Ser	Ala	Ala
			245						250					255	
Phe	Met	Tyr	Ile	Lys	Tyr	Ser	Ser	Gly	Ser	Met	Glu	Gln	Gly	Lys	Val
		260						265					270		
Ser	Ser	Val	Phe	Tyr	Thr	Asn	Val	Val	Pro	Met	Leu	Asn	Pro	Leu	Ile
		275				280					285				
Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Val	Ala	Leu	Arg	Lys	Ala	Leu
	290					295					300				
Ile	Lys	Ile	Gln	Arg	Arg	Asn	Ile	Phe							
305					310										

<210> 31
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 31

```

Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly
 1           5           10           15
Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
      20           25           30
Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
      35           40           45
Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe
      50           55           60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys
      65           70           75           80
Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys
      85           90           95
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr
      100          105          110
Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
      115          120          125
Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Met
      130          135          140
Phe Gly Ser Tyr Val Val Gly Phe Ala Gly Ala Met Ala His Thr Gly
      145          150          155          160
Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn Val Ile Asp His Tyr
      165          170          175
Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr His
      180          185          190
Val Ser Glu Leu Val Phe Phe Ile Val Val Gly Val Ile Thr Met Leu
      195          200          205
Ser Ser Ile Ser Ile Val Ile Ser Tyr Ala Leu Ile Leu Ser Asn Ile
      210          215          220
Leu Cys Ile Pro Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Thr Trp
      225          230          235          240
Gly Ser His Ile Ile Ala Val Ala Leu Phe Phe Gly Ser Gly Thr Phe
      245          250          255
Thr Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met Asn His Gly Arg Phe
      260          265          270
Ala Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Ser Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Asp Asp Lys Leu Ala Leu Gly Lys Thr Leu
      290          295          300
Lys Arg Val Leu Phe
305

```

<210> 32

<211> 762

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (17)...(760)

<400> 32

```

aaatgcctaa agaaga atg acc atg gaa aat tat tct atg gca gct cag ttt
      Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe
      1           5           10

```

52

gtc tta gat ggt tta aca cag caa gca gag ctc cag ctg ccc ctc ttc Val Leu Asp Gly Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe 15 20 25	100
ctc ctg ttc ctg gga atc tat gtg gtc aca gta gtg ggc aac ctg ggc Leu Leu Phe Leu Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly 30 35 40	148
atg att ctc ctg att gca gtc agc cct cta ctt cac acc ccc atg tac Met Ile Leu Leu Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr 45 50 55 60	196
tat ttc ctc agc agc ttg tcc ttc gtc gat ttc tgc tat tcc tct gtc Tyr Phe Leu Ser Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val 65 70 75	244
att act ccc aaa atg ctg gtg aac ttc cta gga aag aag aat aca atc Ile Thr Pro Lys Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile 80 85 90	292
ctt tac tct gag tgc atg gtc cag ctc ttt ttc ttt gtg gtc ttt gtg Leu Tyr Ser Glu Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val 95 100 105	340
gtg gct gag ggt tac ctc ctg act gcc atg gca tat gat cgc tat gtt Val Ala Glu Gly Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val 110 115 120	388
gcc atc tgt agc cca ctg ctt tat aat gcg atc atg tcc tca tgg gtc Ala Ile Cys Ser Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val 125 130 135 140	436
tgc tca ctg cta gtg ctg gct gcc ttc ttc ttg ggc ttt ctc tct gcc Cys Ser Leu Leu Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala 145 150 155	484
ttg act cat aca agt gcc atg atg aaa ctg tcc ttt tgc aaa tcc cac Leu Thr His Thr Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His 160 165 170	532
att atc aac cat tac ttc tgt gat gtt ctt ccc ctc ctc aat ctc tcc Ile Ile Asn His Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser 175 180 185	580
tgc tcc aac aca cac ctc aat gag ctt cta ctt ttt atc att gcg ggg Cys Ser Asn Thr His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly 190 195 200	628
ttt aac acc ttg gtg ccc acc cta gct gtt gct gtc tcc tat gcc ttc Phe Asn Thr Leu Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe 205 210 215 220	676
atc ctc tac agc atc ctt cac atc cgc tcc tca gag ggc cgg tcc aaa Ile Leu Tyr Ser Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys 225 230 235	724
gct ttt gga aca tgc agc tct cat ctc atg gct gtg gt	762

Ala Phe Gly Thr Cys Ser Ser His Leu Met Ala Val
 240 245

<210> 33
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly
 1 5 10 15
 Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu
 35 40 45
 Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu
 85 90 95
 Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly
 100 105 110
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser
 115 120 125
 Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu
 130 135 140
 Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr
 145 150 155 160
 Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His
 165 170 175
 Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr
 180 185 190
 His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu
 195 200 205
 Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser
 210 215 220
 Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Ser Ser His Leu Met Ala Val
 245

<210> 34
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 34
 gaagagcagt gaggggtccat gttaagg

27

<210> 35
 <211> 28
 <212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 35

cagcagcttg tccttcgtcg atttctgc

28

<210> 36

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 36

gctaggggtgg gcaccaaggt gttaaacc

29

<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 37

tgcaaaagga cagtttcatc atggcac

27

<210> 38

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 38

caaagaactc acccaaattc ctacagct

28

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 39

catggtaggc aaccttggct tgatcac

27

<210> 40

<211> 29

<212> DNA

<213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 40
 gtttattaaa tcacacataa caccatctg 29

<210> 41
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 41
 cagagacaga gcaatgacat gagagctac 29

<210> 42
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 42
 caaagaactc acccaaattc ctacagcc 28

<210> 43
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 43
 catggtaggc aaccttggct tgatcat 27

<210> 44
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 44
 gtttattaaa tcacacataa caccatctg 29

<210> 45
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized Primer Sequence

<400> 45
 cagagacaga gcaatgacat gagagctac 29

 <210> 46
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 46
 ccagacagct cgccaagaga gaatgac 27

 <210> 47
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 47
 cctttataga tctctgttat tcctgtgtg 29

 <210> 48
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 48
 tcggttgcca gtgatatgaa gagaccc 27

 <210> 49
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized Primer Sequence

 <400> 49
 ggctttggat ctgccctctg cagaagg 27

 <210> 50
 <211> 450
 <212> DNA
 <213> Homo sapiens

 <400> 50
 cagcagcttg tccttcgtcg atttctgcta ttcctctgtc attactccca aaatgctggt 60
 gaacttccta ggaaagaaga atacaatcct ttactctgag tgcattgtcc agctcttttt 120
 ctttctggtc tttgtggtgg ctgagggtta cctcctgact gccatggcat atgatcgcta 180

tggtgccatc	tgtagcccac	tgctttataa	tgcgatcatg	tcctcatggg	tctgctcact	240
gctagtgcctg	gctgccttct	tcttgggctt	tctctctgcc	ttgactcata	caagtgccat	300
gatgaaactg	tccttttgca	aatccacat	tatcaaccat	tacttctgtg	atgttcttcc	360
cctcctcaat	ctctcctgct	ccaacacaca	cctcaatgag	cttctacttt	ttatcattgc	420
ggggtttaac	accttggtgc	ccaccctagc				450

<210> 51
 <211> 637
 <212> DNA
 <213> Homo sapiens

<400> 51						
catggtaggc	aaccttggtc	tgatcactct	tttcgggtcta	aattctcacc	tccacacacc	60
aatgtactat	ttcctcttca	atctctcctt	cattgatctc	tgttactcct	ctgttttcac	120
tcccaaaatg	ctaatagaact	ttgtgtcaaa	aaagaatatt	atctccaatg	ttgggtgcat	180
gactcggctg	tttttctttc	tctttttcgt	catctctgaa	tgttacatgt	tgacctcaat	240
ggcatatgat	cgctatgtgg	ccatctgtaa	tccattgctg	tataagggtca	ccatgtccca	300
tcaggctctgt	tctatgctca	cttttgctgc	ttacataatg	ggattggctg	gagccaaggc	360
ccacaccggg	tgcatgttta	gactcacctt	ctgcagtgtc	aatatcatta	accattactt	420
gtgtgacata	ctccccctcc	tccagctttc	ctgcaccagc	acctatgtca	acgagggtgt	480
tgttctcatt	gttgtgggta	ctaataacac	ggtagccagt	tgtaccatcc	tcatttctta	540
tgttttcatt	gtcactagca	ttcttcatat	caaattccact	caaggaagat	caaaagcctt	600
cagtacttgt	agctctcatg	tcattgctct	gtctctg			637

<210> 52
 <211> 637
 <212> DNA
 <213> Homo sapiens

<400> 52						
catggtaggc	aaccttggtc	tgatcattct	tttcgggtcta	aattctcacc	tccacacacc	60
aatgtactat	ttcctcttca	atctctcctt	cattgatctc	tgttactcct	ctgttttcac	120
tcccaaaatg	ctaatagaact	ttgtatcaaa	aaagaatatt	atctcctatg	ttgggtgcat	180
gactcagctg	tttttctttc	tcttttttgt	catctctgaa	tgctacatat	tgacctcaat	240
ggcatatgat	cgctatgtgg	ccatctgtaa	tccattgctg	tataagggtca	ccatgtccca	300
tcaggctctgt	tctatgctca	cttttgctgc	ttacataatg	ggattggctg	gagccacggc	360
ccacaccggg	tgcatgttta	gactcacctt	ctgcagtgtc	aatatcatca	accattactt	420
gtgtgacata	ctccccctcc	tccagctttc	ctgcaccagc	acctatgtca	acgagggtgt	480
tgttctcatt	gttgtgggta	ttaatatcat	ggtagccagt	tgtaccatcc	tcatttctta	540
tgttttcatt	gtcactagca	ttcttcatat	caaattccact	caaggaagat	caaaagcctt	600
cagtacttgt	agctctcatg	tcattgctct	gtctctg			637

<210> 53
 <211> 509
 <212> DNA
 <213> Homo sapiens

<400> 53						
cctttataga	tctctgttat	tctgtgtgt	ttacccccaa	aatgctgaat	gactttgttt	60
cagaaagtat	catctcttat	gtgggatgta	tgactcagct	atttttcttc	tgtttctttg	120
tcaattctga	gtgctatgtg	ttggtatcaa	tggcctatga	tcgctatgtg	gccatctgca	180
acccccctgt	ctacatggtc	accatgtccc	caagggtctg	ctttctgctg	atgtttgggt	240
cctatgtggt	aggggttgct	ggggccatgg	cccacactgg	aagcatgctg	cgactgacct	300
tctgtgattc	caacgtcatt	gaccattatc	tgtgtgacgt	tctccccctc	ttgcagctct	360
cctgcaccag	cacccatgtc	agtgaagctg	tatttttcat	tgttgttgga	gtaatcacca	420
tgctatccag	cataagcatc	gtcatctctt	acgctttgat	actctccaac	atcctctgta	480
ttccttctgc	agagggcaga	tccaaagcc				509

<210> 54
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Exemplary motif

<221> VARIANT
 <222> 7
 <223> Xaa = Leu or Val

<221> VARIANT
 <222> 9
 <223> Xaa = Ile or Val

<400> 54
 Met Ala Tyr Asp Arg Tyr Xaa Ala Xaa Cys
 1 5 10

<210> 55
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 55
 Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 1 5 10

<210> 56
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys
 1 5 10

<210> 57
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 57
 Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe
 1 5 10

<210> 58
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Glu Phe Thr Asp Arg Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu
 1 5 10 15
 Leu Gly Phe Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Met

二、三、四

<400> 59															
Met	Asp	Asn	Gln	Ser	Ser	Thr	Pro	Gly	Phe	Leu	Leu	Leu	Gly	Phe	Ser
1				5					10					15	
Glu	His	Pro	Gly	Leu	Gly	Arg	Thr	Leu	Phe	Val	Asp	Val	Ile	Thr	Ser
			20					25					30		
Tyr	Leu	Leu	Thr	Leu	Val	Gly	Asn	Thr	Leu	Ile	Ile	Leu	Leu	Ser	Ala
		35				40						45			
Leu	Asp	Thr	Lys	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Ser	Asn	Leu
	50					55				60					
Ser	Phe	Leu	Asp	Leu	Cys	Phe	Thr	Thr	Ser	Cys	Val	Pro	Gln	Met	Leu
65					70					75					80
Ala	Asn	Leu	Trp	Gly	Pro	Lys	Lys	Thr	Ile	Ser	Phe	Leu	Asp	Cys	Ser
				85					90					95	
Val	Gln	Ile	Phe	Ile	Phe	Leu	Ser	Leu	Gly	Thr	Thr	Glu	Cys	Ile	Leu

```
<210> 60
<211> 317
<212> PRT
<213> Homo sapiens
```

<400>	60														
Met	Gly	Thr	Asp	Asn	Gln	Thr	Trp	Val	Ser	Glu	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Leu	Ser	Ser	Asp	Trp	Asp	Thr	Arg	Val	Ser	Leu	Phe	Val	Leu	Phe	Leu
			20					25					30		
Val	Met	Tyr	Val	Val	Thr	Val	Leu	Gly	Asn	Cys	Leu	Ile	Val	Leu	Leu
		35					40					45			
Ile	Arg	Leu	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr
	50					55					60				
Asn	Leu	Ser	Leu	Val	Asp	Val	Ser	Tyr	Ala	Thr	Ser	Val	Val	Pro	Gln
65					70					75				80	
Leu	Leu	Ala	His	Phe	Leu	Ala	Glu	His	Lys	Ala	Ile	Pro	Phe	Gln	Ser
				85					90					95	
Cys	Ala	Ala	Gln	Leu	Phe	Phe	Ser	Leu	Ala	Leu	Gly	Gly	Ile	Glu	Phe
			100					105					110		
Val	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Val	Cys	Asp
		115					120					125			
Ala	Leu	Arg	Tyr	Ser	Ala	Ile	Met	His	Gly	Gly	Leu	Cys	Ala	Arg	Leu
		130				135					140				
Ala	Ile	Thr	Ser	Trp	Val	Ser	Gly	Phe	Ile	Ser	Ser	Pro	Val	Gln	Thr
145					150					155				160	
Ala	Ile	Thr	Phe	Gln	Leu	Pro	Met	Cys	Arg	Asn	Lys	Phe	Ile	Asp	His
				165					170					175	
Ile	Ser	Cys	Glu	Leu	Leu	Ala	Val	Val	Arg	Leu	Ala	Cys	Val	Asp	Thr

			180					185				190			
Ser	Ser	Asn	Glu	Val	Thr	Ile	Met	Val	Ser	Ser	Ile	Val	Leu	Leu	Met
		195					200					205			
Thr	Pro	Leu	Cys	Leu	Val	Leu	Leu	Ser	Tyr	Ile	Gln	Ile	Ile	Ser	Thr
	210					215					220				
Ile	Leu	Lys	Ile	Gln	Ser	Arg	Glu	Gly	Arg	Lys	Lys	Ala	Phe	His	Thr
225					230					235					240
Cys	Ala	Ser	His	Leu	Thr	Val	Val	Ala	Leu	Cys	Tyr	Gly	Val	Ala	Ile
			245						250					255	
Phe	Thr	Tyr	Ile	Gln	Pro	His	Ser	Ser	Pro	Ser	Val	Leu	Gln	Glu	Lys
			260					265					270		
Leu	Phe	Ser	Val	Phe	Tyr	Ala	Ile	Leu	Thr	Pro	Met	Leu	Asn	Pro	Met
		275					280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Trp	Gln	Lys	Leu
	290				295						300				
Leu	Trp	Lys	Phe	Ser	Gly	Leu	Thr	Ser	Lys	Leu	Ala	Thr			
305					310						315				

<210> 61

<211> 315

<212> PRT

<213> Homo sapiens

<400> 61

Met	Glu	Glu	Ala	Ile	Leu	Leu	Asn	Gln	Thr	Ser	Leu	Val	Thr	Tyr	Phe
1				5					10					15	
Arg	Leu	Arg	Gly	Leu	Ser	Val	Asn	His	Lys	Ala	Arg	Ile	Ala	Met	Phe
			20					25					30		
Ser	Met	Phe	Leu	Ile	Phe	Tyr	Val	Leu	Thr	Leu	Ile	Gly	Asn	Val	Leu
		35					40					45			
Ile	Val	Ile	Thr	Ile	Ile	Tyr	Asp	His	Arg	Leu	His	Thr	Pro	Met	Tyr
	50					55					60				
Phe	Phe	Leu	Ser	Asn	Leu	Ser	Phe	Ile	Asp	Val	Cys	His	Ser	Thr	Val
65				70					75						80
Thr	Val	Pro	Lys	Met	Leu	Arg	Asp	Val	Trp	Ser	Glu	Glu	Lys	Leu	Ile
			85						90					95	
Ser	Phe	Asp	Ala	Cys	Val	Thr	Gln	Met	Phe	Phe	Leu	His	Leu	Phe	Ala
			100					105					110		
Cys	Thr	Glu	Ile	Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val
		115					120					125			
Ala	Ile	Cys	Lys	Pro	Leu	Gln	Tyr	Met	Ile	Val	Met	Asn	Trp	Lys	Val
	130					135					140				
Cys	Val	Leu	Leu	Ala	Val	Ala	Leu	Trp	Thr	Gly	Gly	Thr	Ile	His	Ser
145				150						155					160
Ile	Ala	Leu	Thr	Ser	Leu	Thr	Ile	Lys	Leu	Pro	Tyr	Cys	Gly	Pro	Asp
			165					170						175	
Glu	Ile	Asp	Asn	Phe	Phe	Cys	Asp	Val	Pro	Gln	Val	Ile	Lys	Leu	Ala
		180					185					190			
Cys	Ile	Asp	Thr	Pro	Thr	Ser	Leu	Ile	Leu	Ile	Val	Ser	Asn	Ser	Gly
		195					200					205			
Leu	Ile	Ser	Val	Val	Cys	Phe	Val	Val	Leu	Val	Val	Ser	Tyr	Ala	Val
	210					215					220				
Ile	Leu	Val	Ser	Leu	Arg	Gln	Gln	Ile	Ser	Lys	Gly	Lys	Trp	Lys	Ala
225					230					235					240
Leu	Ser	Thr	Cys	Ala	Ala	His	Leu	Thr	Val	Val	Thr	Leu	Phe	Leu	Gly
			245						250					255	
His	Cys	Ile	Phe	Ile	Tyr	Ser	Arg	Pro	Ser	Thr	Ser	Leu	Pro	Glu	Asp


```
<210> 62
<211> 313
<212> PRT
<213> Homo sapiens
```

<400>	62														
Met 1	Gly	Lys	Thr	Lys 5	Asn	Thr	Ser	Leu	Asp 10	Thr	Val	Val	Arg 15	Asp	Phe
Ile	Leu	Leu	Gly 20	Leu	Ser	His	Pro	Pro 25	Asn	Ile	Arg	Ser	Leu 30	Leu	Phe
Leu	Val	Phe 35	Phe	Val	Ile	Tyr	Ile 40	Leu	Thr	Gln	Leu	Gly 45	Asn	Leu	Leu
Ile 50	Leu	Leu	Thr	Val	Trp	Ala 55	Asp	Pro	Lys	Leu	Arg 60	Ala	Arg	Pro	Met
Tyr 65	Ile	Leu	Leu	Gly 70	Val	Leu	Ser	Phe	Leu	Asp 75	Met	Trp	Leu	Ser	Ser
Val	Ile	Val	Pro	Ile 85	Ile	Leu	Asn	Pro	Thr 90	Pro	Ala	Asn	Lys 95	Ala	Ile
Pro	Phe	Gly 100	Gly	Cys	Val	Ala	Gln	Leu 105	Tyr	Phe	Phe	His 110	Phe	Leu	Gly
Ser	Thr	Gln 115	Cys	Phe	Leu	Tyr	Thr 120	Leu	Met	Ala	Tyr	Asp 125	Arg	Tyr	Leu
Ala 130	Ile	Cys	Gln	Pro	Leu	Arg 135	Tyr	Pro	Val	Leu	Met 140	Asn	Gly 145	Arg	Leu
Cys 145	Thr	Val	Leu	Val	Ala 150	Gly	Ala	Trp	Val	Ala 155	Gly	Ser	Met 160	His	Gly
Ser	Ile	Gln	Ala	Thr 165	Leu	Thr	Phe	Arg 170	Leu	Pro	Tyr	Cys 175	Gly	Pro	Asn
Gln	Val	Asp	Tyr 180	Phe	Ile	Cys	Asp 185	Ile	Pro	Ala	Val	Leu 190	Arg	Leu	Ala
Cys	Ala	Asp 195	Thr	Thr	Val	Asn 200	Glu	Leu	Val	Thr	Phe 205	Val	Asp 210	Ile	Gly
Val 210	Val	Ala	Ala	Ser	Cys 215	Phe	Met	Leu	Ile	Leu 220	Leu	Ser	Tyr 225	Ala	Asn
Ile 225	Val	Asn	Ala	Ile 230	Leu	Lys	Ile	Arg	Thr 235	Thr	Asp	Gly	Arg 240	Arg	Arg
Ala	Phe	Ser	Thr	Cys 245	Gly	Ser	His	Leu	Ile 250	Val	Val	Thr 255	Val	Tyr	Tyr
Val	Pro	Cys	Ile 260	Phe	Ile	Tyr	Leu 265	Arg	Ala	Gly	Ser	Lys 270	Gly	Pro	Leu
Asp	Gly	Ala 275	Ala	Ala	Val	Phe 280	Tyr	Thr	Val	Val	Thr 285	Pro	Leu 290	Leu	Asn
Pro	Leu 290	Ile	Tyr	Thr	Leu	Arg 295	Asn	Gln	Glu	Val	Lys 300	Ser	Ala	Leu	Lys
Arg 305	Ile	Thr	Ala	Gly 310	Gln	Gly	Thr	Glu							